



IFWO

RAW SEQUENCE LISTING

DATE: 09/03/2004

PATENT APPLICATION: US/10/627,649

TIME: 15:21:34

Input Set : A:\10 627,649 Sequence Listing.txt

Output Set: N:\CRF4\09032004\J627649.raw

3 <110> APPLICANT: EDELMAN, LENA
 4 JACOTOT, ETIENNE DANIEL FRANCOIS
 5 BRIAND, JEAN-PAUL
 7 <120> TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
 8 SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC
 9 FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
 10 (PTPC)
 12 <130> FILE REFERENCE: 02356-0083
 14 <140> CURRENT APPLICATION NUMBER: 10/627,649
 15 <141> CURRENT FILING DATE: 2003-07-28
 17 <150> PRIOR APPLICATION NUMBER: 60/265,594
 18 <151> PRIOR FILING DATE: 2001-02-02
 20 <160> NUMBER OF SEQ ID NOS: 325
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 10517
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: Description of Artificial Sequence: vector pACgp67-ScFv461
 31 nucleotide sequence
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (1)..(10515)
 37 <400> SEQUENCE: 1
 38 aag ctt tac tcg taa agc gag ttg aag gat cat att tag ttg cgt tta 48
 39 Lys Leu Tyr Ser Ser Glu Leu Lys Asp His Ile Leu Arg Leu
 40 1 5 10
 42 tga gat aag att gaa agc acg tgt aaa atg ttt ccc gcg cgt tgg cac 96
 43 Asp Lys Ile Glu Ser Thr Cys Lys Met Phe Pro Ala Arg Trp His
 44 15 20 25
 46 aac tat tta caa tgc ggc caa gtt ata aaa gat tct aat ctg ata tgt 144
 47 Asn Tyr Leu Gln Cys Gly Gln Val Ile Lys Asp Ser Asn Leu Ile Cys
 48 30 35 40 45
 50 ttt aaa aca cct ttg cgg ccc gag ttg ttt gcg tac gtg act agc gaa 192
 51 Phe Lys Thr Pro Leu Arg Pro Glu Leu Phe Ala Tyr Val Thr Ser Glu
 52 50 55 60
 54 gaa gat gtg tgg acc gca gaa cag ata gta aaa caa aac cct agt att 240
 55 Glu Asp Val Trp Thr Ala Glu Gln Ile Val Lys Gln Asn Pro Ser Ile
 56 65 70 75
 58 gga gca ata atc gat tta acc aac acg tct aaa tat tat gat ggt gtg 288
 59 Gly Ala Ile Ile Asp Leu Thr Asn Thr Ser Lys Tyr Tyr Asp Gly Val
 60 80 85 90



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62	cat	ttt	ttg	cgg	gcg	ggc	ctg	tta	tac	aaa	aaa	att	caa	gta	cct	ggc	336
63	His	Phe	Leu	Arg	Ala	Gly	Leu	Leu	Tyr	Lys	Lys	Ile	Gln	Val	Pro	Gly	
64	95					100						105					
66	cag	act	ttg	cgg	cct	gaa	agc	ata	ggt	caa	gaa	ttt	att	gac	acg	gta	384
67	Gln	Thr	Leu	Pro	Pro	Glu	Ser	Ile	Val	Gln	Glu	Phe	Ile	Asp	Thr	Val	
68	110					115						120				125	
70	aaa	gaa	ttt	aca	gaa	aag	tgt	ccc	ggc	atg	ttg	gtg	ggc	gtg	cac	tgc	432
71	Lys	Glu	Phe	Thr	Glu	Lys	Cys	Pro	Gly	Met	Leu	Val	Gly	Val	His	Cys	
72						130				135					140		
74	aca	cac	ggt	att	aat	cgc	acc	ggt	tac	atg	gtg	tgc	aga	tat	tta	atg	480
75	Thr	His	Gly	Ile	Asn	Arg	Thr	Gly	Tyr	Met	Val	Cys	Arg	Tyr	Leu	Met	
76						145				150					155		
78	cac	acc	ctg	ggt	att	gcg	ccg	cag	gaa	gcc	ata	gat	aga	ttc	gaa	aaa	528
79	His	Thr	Leu	Gly	Ile	Ala	Pro	Gln	Glu	Ala	Ile	Asp	Arg	Phe	Glu	Lys	
80						160				165				170			
82	gcc	aga	ggt	cac	aaa	att	gaa	aga	caa	aat	tac	ggt	caa	gat	tta	tta	576
83	Ala	Arg	Gly	His	Lys	Ile	Glu	Arg	Gln	Asn	Tyr	Val	Gln	Asp	Leu	Leu	
84	175					180						185					
86	att	taa	tta	ata	tta	ttt	gca	ttc	ttt	aac	aaa	tac	ttt	atc	cta	ttt	624
87	Ile		Leu	Ile	Leu	Phe	Ala	Phe	Phe	Asn	Lys	Tyr	Phe	Ile	Leu	Phe	
88	190					195						200					
90	tca	aat	tgt	tgc	gct	tct	tcc	agc	gaa	cca	aaa	cta	tgc	ttc	gct	tgc	672
91	Ser	Asn	Cys	Cys	Ala	Ser	Ser	Ser	Glu	Pro	Lys	Leu	Cys	Phe	Ala	Cys	
92	205					210						215			220		
94	tcc	ggt	tag	ctt	gta	gcc	gat	cag	tgg	cgt	tgt	tcc	aat	cga	cgg	tag	720
95	Ser	Val		Leu	Val	Ala	Asp	Gln	Trp	Arg	Cys	Ser	Asn	Arg	Arg		
96						225						230					
98	gat	tag	gcc	gga	tat	tct	cca	cca	caa	tgt	tgg	caa	cgt	tga	tgt	tac	768
99	Asp		Ala	Gly	Tyr	Ser	Pro	Pro	Gln	Cys	Trp	Gln	Arg		Cys	Tyr	
100	235					240						245					
102	ggt	tat	gct	ttt	ggt	ttt	cca	cgt	acg	tct	ttt	ggc	cgg	taa	tag	ccg	816
103	Val	Tyr	Ala	Phe	Gly	Phe	Pro	Arg	Thr	Ser	Phe	Gly	Arg		Pro		
104						250						255			260		
106	taa	acg	tag	tgc	cgt	cgc	tca	cgc	aca	aca	ccg	gat	ggt	tgc	gct		864
107	Thr			Cys	Arg	Arg	Ala	Ser	Arg	Thr	Thr	Pro	Asp	Val	Cys	Ala	
108						265						270			275		
110	tgt	ccg	cgg	ggt	att	gaa	ccg	cgc	gat	ccg	aca	aat	cca	cca	ctt	tgg	912
111	Cys	Pro	Arg	Gly	Ile	Glu	Pro	Arg	Asp	Pro	Thr	Asn	Pro	Pro	Leu	Trp	
112						280						285			290		
114	caa	cta	aat	cgg	tga	cct	gcg	cgt	ctt	ttt	tct	gca	tta	ttt	cgt	ctt	960
115	Gln	Leu	Asn	Arg		Pro	Ala	Arg	Leu	Phe	Ser	Ala	Leu	Phe	Arg	Leu	
116						295						300			305		
118	tct	ttt	gca	tgg	ttt	cct	gga	agc	cgg	tgt	aca	tgc	ggt	tta	gat	cag	1008
119	Ser	Phe	Ala	Trp	Phe	Pro	Gly	Ser	Arg	Cys	Thr	Cys	Gly	Leu	Asp	Gln	
120						310						315			320		
122	tca	tga	cgc	gcg	tga	cct	gca	aat	ctt	tgg	cct	cga	tct	gct	tgt	cct	1056
123	Ser		Arg	Ala		Pro	Ala	Asn	Leu	Trp	Pro	Arg	Ser	Ala	Cys	Pro	
124						325						330			335		
126	tga	tgg	caa	cga	tgc	ggt	caa	taa	act	ctt	ggt	ttt	taa	caa	ggt	cct	1104

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127	Trp	Gln	Arg	Cys	Val	Gln	Thr	Leu	Val	Phe	Gln	Val	Pro				
128			340					345					350				
130	cgg	ttt	ttt	gcg	cca	cca	ccg	ctt	gca	gcg	cgt	ttg	tgt	gct	cgg	tga	1152
131	Arg	Phe	Phe	Ala	Pro	Pro	Pro	Leu	Ala	Ala	Arg	Leu	Cys	Ala	Arg		
132				355					360					365			
134	atg	tcg	caa	tca	gct	tag	tca	cca	act	gtt	tgc	tct	cct	cct	ccc	gtt	1200
135	Met	Ser	Gln	Ser	Ala		Ser	Pro	Thr	Val	Cys	Ser	Pro	Pro	Pro	Val	
136				370							375					380	
138	gtt	tga	tcg	cgg	gat	cgt	act	tgc	cgg	tgc	aga	gca	ctt	gag	gaa	tta	1248
139	Val		Ser	Arg	Asp	Arg	Thr	Cys	Arg	Cys	Arg	Ala	Leu	Glu	Glu	Leu	
140					385						390					395	
142	ctt	ctt	cta	aaa	gcc	att	ctt	gta	att	cta	tgg	cgt	aag	gca	att	tgg	1296
143	Leu	Leu	Leu	Lys	Ala	Ile	Leu	Val	Ile	Leu	Trp	Arg	Lys	Ala	Ile	Trp	
144				400						405					410		
146	act	tca	taa	tca	gct	gaa	tca	cgc	cgg	att	tag	taa	tga	gca	ctg	tat	1344
147	Thr	Ser		Ser	Ala	Glu	Ser	Arg	Arg	Ile				Ala	Leu	Tyr	
148				415						420							
150	gcg	gct	gca	aat	aca	gcg	ggg	cgc	ccc	ttt	tca	cga	cgc	tgt	tag	agg	1392
151	Ala	Ala	Ala	Asn	Thr	Ala	Gly	Arg	Pro	Phe	Ser	Arg	Arg	Cys		Arg	
152		425				430				435							
154	tag	ggc	ccc	cat	ttt	gga	tgg	tct	gct	caa	ata	acg	att	tgt	att	tat	1440
155		Gly	Pro	His	Phe	Gly	Trp	Ser	Ala	Gln	Ile	Thr	Ile	Cys	Ile	Tyr	
156			440				445				450						
158	tgt	cta	cat	gaa	cac	gta	tag	ctt	tat	cac	aaa	ctg	tat	att	tta	aac	1488
159	Cys	Leu	His	Glu	His	Val		Leu	Tyr	His	Lys	Leu	Tyr	Ile	Leu	Asn	
160		455					460				465						
162	tgt	tag	cga	cgt	cct	tgg	cca	cga	acc	gga	cct	gtt	ggg	cgc	gct	cta	1536
163	Cys		Arg	Arg	Pro	Trp	Pro	Arg	Thr	Gly	Pro	Val	Gly	Arg	Ala	Leu	
164			470				475				480						
166	gca	cgt	acc	gca	ggg	tga	acg	tat	ctt	ctc	caa	att	taa	att	ctc	caa	1584
167	Ala	Arg	Thr	Ala	Gly		Thr	Tyr	Leu	Leu	Gln	Ile		Ile	Leu	Gln	
168		485					490				495						
170	ttt	taa	cgc	gag	cca	ttt	tga	tac	acg	tgt	gtc	gat	ttt	gca	aca	act	1632
171	Phe		Arg	Glu	Pro	Phe		Tyr	Thr	Cys	Val	Asp	Phe	Ala	Thr	Thr	
172			500							505					510		
174	att	gtt	ttt	taa	cgc	aaa	cta	aac	tta	ttg	tgg	taa	gca	ata	att	aaa	1680
175	Ile	Val	Phe		Arg	Lys	Leu	Asn	Leu	Leu	Trp		Ala	Ile	Ile	Lys	
176				515						520						525	
178	tat	ggg	gga	aca	tgc	gcc	gct	aca	aca	ctc	gtc	gtt	atg	aac	gca	gac	1728
179	Tyr	Gly	Gly	Thr	Cys	Ala	Ala	Thr	Thr	Leu	Val	Val	Met	Asn	Ala	Asp	
180				530						535					540		
182	ggc	gcc	ggg	ctc	ggc	gca	agc	ggc	taa	aac	gtg	ttg	cgc	gtt	caa	cgc	1776
183	Gly	Ala	Gly	Leu	Gly	Ala	Ser	Gly		Asn	Val	Leu	Arg	Val	Gln	Arg	
184				545						550					555		
186	ggc	aaa	cat	cgc	aaa	agc	caa	tag	tac	agt	ttt	gat	ttg	cat	att	aac	1824
187	Gly	Lys	His	Arg	Lys	Ser	Gln		Tyr	Ser	Phe	Asp	Leu	His	Ile	Asn	
188				560						565					570		
190	ggc	gat	ttt	taa	aat	tat	ctt	att	taa	taa	ata	gtt	atg	acg	cct	aca	1872
191	Gly	Asp	Phe	Leu	Asn	Tyr	Leu	Ile			Ile	Val	Met	Thr	Pro	Thr	

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192		575		580		585	
194	act	ccc	cgc	ccg	cgt	tga	ctc
195	Thr	Pro	Arg	Pro	Arg	Leu	Ala
196				590		595	
198	ctt	cct	ccg	tgt	ggc	cga	aca
199	Leu	Pro	Pro	Cys	Gly	Arg	Thr
200	600			605		610	
202	gcg	tgc	cgc	acg	cga	cgc	aca
203	Ala	Cys	Arg	Thr	Arg	Arg	Thr
204	615			620		625	
206	gcg	aag	gca	cgt	cgg	cct	cca
207	Ala	Lys	Ala	Arg	Arg	Pro	Pro
208				635		640	
210	ata	tac	agt	tgg	gtt	gtt	tgc
211	Ile	Tyr	Ser	Trp	Val	Val	Cys
212				650		655	
214	acg	tcc	gaa	cgt	tga	ttt	gca
215	Thr	Ser	Glu	Arg		Phe	Ala
216				665		670	
218	tag	tgc	gat	taa	aac	gtt	gta
219		Cys	Asp		Asn	Val	Val
220				680		685	
222	tta	aat	cgc	gca	atc	gag	tca
223	Leu	Asn	Arg	Ala	Ile	Glu	Ser
224				695		700	
226	ctt	tgt	att	ccc	gag	tca	agc
227	Leu	Cys	Ile	Pro	Glu	Ser	Ser
228				710		715	
230	tct	tgt	aag	tta	gtt	tca	ttt
231	Ser	Cys	Lys	Leu	Val	Ser	Phe
232				725		730	
234	tgt	atc	gca	cgt	caa	gaa	tta
235	Cys	Ile	Ala	Arg	Gln	Glu	Leu
236				740		745	
238	acg	act	atg	ata	gag	atc	aaa
239	Thr	Thr	Met	Ile	Glu	Ile	Lys
240				755		760	
242	gca	acg	tgc	acg	atc	tgt	gca
243	Ala	Thr	Cys	Thr	Ile	Cys	Ala
244				770		775	
246	ata	agt	ttt	tac	gaa	gcg	atg
247	Ile	Ser	Phe	Tyr	Glu	Ala	Met
248				785		790	
250	cgc	cca	aaa	gaa	ctg	ccg	act
251	Arg	Pro	Lys	Glu	Leu	Pro	Thr
252				800		805	
254	tta	aaa	cta	tta	agc	cat	cca
255	Leu	Lys	Leu	Leu	Ser	His	Pro
256				815		820	

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258	tgg tgc gag aag ccg cga agt atg gcg aat gca tcg tat aac gtg tgg	2688
259	Trp Cys Glu Lys Pro Arg Ser Met Ala Asn Ala Ser Tyr Asn Val Trp	
260	830 835 840	
262	agt ccg ctc att aga gcg tca tgt tta gac aag aaa gct aca tat tta	2736
263	Ser Pro Leu Ile Arg Ala Ser Cys Leu Asp Lys Lys Ala Thr Tyr Leu	
264	845 850 855	
266	att gat ccc gat gat ttt att gat aaa ttg acc cta act cca tac acg	2784
267	Ile Asp Pro Asp,Asp Phe Ile Asp Lys Leu Thr Leu Thr Pro Tyr Thr	
268	860 865 870	
270	gta ttc tac aat ggc ggg gtt ttg gtc aaa att tcc gga ctg cga ttg	2832
271	Val Phe Tyr Asn Gly Gly Val Leu Val Lys Ile Ser Gly Leu Arg Leu	
272	875 880 885 890	
274	tac atg ctg tta acg gct ccg ccc act att aat gaa att aaa aat tcc	2880
275	Tyr Met Leu Leu Thr Ala Pro Pro Thr Ile Asn Glu Ile Lys Asn Ser	
276	895 900 905	
278	aat ttt aaa aaa cgc agc aag aga aac att tgt atg aaa gaa tgc gta	2928
279	Asn Phe Lys Lys Arg Ser Lys Arg Asn Ile Cys Met Lys Glu Cys Val	
280	910 915 920	
282	gaa gga aag aaa aat gtc gtc gac atg ctg aac aac aag att aat atg	2976
283	Glu Gly Lys Lys Asn Val Val Asp Met Leu Asn Asn Lys Ile Asn Met	
284	925 930 935	
286	cct ccg tgt ata aaa aaa ata ttg aac gat ttg aaa gaa aac aat gta	3024
287	Pro Pro Cys Ile Lys Lys Ile Leu Asn Asp Leu Lys Glu Asn Asn Val	
288	940 945 950	
290	ccg cgc ggc ggt atg tac agg aag agg ttt ata cta aac tgt tac att	3072
291	Pro Arg Gly Gly Met Tyr Arg Lys Arg Phe Ile Leu Asn Cys Tyr Ile	
292	955 960 965 970	
294	gca aac gtg gtt tcg tgt gcc aag tgt gaa aac cga tgt tta atc aag	3120
295	Ala Asn Val Val Ser Cys Ala Lys Cys Glu Asn Arg Cys Leu Ile Lys	
296	975 980 985	
298	gct ctg acg cat ttc tac aac cac gac tcc aag tgt gtg ggt gaa gtc	3168
299	Ala Leu Thr His Phe Tyr Asn His Asp Ser Lys Cys Val Gly Glu Val	
300	990 995 1000	
302	atg cat ctt tta atc aaa tcc caa gat gtg tat aaa cca cca aac	3213
303	Met His Leu Leu Ile Lys Ser Gln Asp Val Tyr Lys Pro Pro Asn	
304	1005 1010 1015	
306	tgc caa aaa atg aaa act gtc gac aag ctc tgt ccg ttt gct ggc	3258
307	Cys Gln Lys Met Lys Thr Val Asp Lys Leu Cys Pro Phe Ala Gly	
308	1020 1025 1030	
310	aac tgc aag ggt ctc aat cct att tgt aat tat tga ata ata aaa	3303
311	Asn Cys Lys Gly Leu Asn Pro Ile Cys Asn Tyr Ile Ile Lys	
312	1035 1040 1045	
314	caa tta taa atg cta aat ttg ttt ttt att aac gat aca aac caa	3348
315	Gln Leu Met Leu Asn Leu Phe Phe Ile Asn Asp Thr Asn Gln	
316	1050 1055 1060	
318	acg caa caa gaa cat ttg tag tat tat cta taa ttg aaa acg cgt agt	3396
319	Thr Gln Gln Glu His Leu Tyr Tyr Leu Leu Lys Thr Arg Ser	
320	1065 1070	
322	tat aat cgc tga ggt aat att taa aat cat ttt caa atg att cac	3441

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:273; Xaa Pos. 2

VERIFICATION SUMMARY

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L:6860 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:273 after pos.:0